Program/Abstract # 484
Global analysis of the LEAFY transcriptional network: Transitioning to reproductive development in *Arabidopsis thaliana*
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The transition from vegetative to reproductive development in *Arabidopsis thaliana* involves the integration of multiple environmental and endogenous cues and the translation of these cues into the developmental program of flower-morphogenesis. The LEAFY (LFY) transcription factor has been identified as the key integrator and master regulator of this transition. In addition to its role in the initiation of floral development during the meristem identity (MI) transition, LFY also has a later role in the induction of homeotic genes that specify floral organ identity (i.e. floral patterning). Using a post-translationally activatable form of LFY, a ChIP-on-chip approach was taken to identify targets of LFY during the initiation of flower development. Preliminary analyses suggest that LFY binds to over 1000 targets, suggesting it plays a large role in the transition to reproductive development in *Arabidopsis*. All known MI regulators were identified as LFY targets in this dataset. In addition, new potential LFY targets include genes involved in leaf development, hormone signaling, chromatin remodeling, and flowering time, suggesting a link between meristem identity and these pathways.

doi:10.1016/j.ydbio.2008.05.465

Program/Abstract # 485
The histone acetyltransferase GCN5 affects floral bud initiation and stamen development in *Arabidopsis*
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A central question in biology is to understand how gene expression is precisely regulated to give rise to a variety of forms during the process of development. Epigenetic effects such as DNA methylation or histone modification have been increasingly shown to play a critical role in regulation of genome function. GCN5 is prototypical histone acetyltransferase that has been shown to participate in regulating developmental gene expression in a several metazoan species. In *Arabidopsis*, plants with T-DNA insertions in *GCN5* (also known as *HAG1*) display a variety of pleiotropic effects including dwarfism, loss of apical dominance, and floral defects affecting fertility. We sought to determine when during early development these floral defects first arise. Using scanning electron microscopy, we demonstrate that *gcn5-1/hag 1-1* and *gcn5-4/hag1-5* mutants display abnormal proliferation of young buds around the floral meristem as well as defects in stamen number and arrangement at later stages. This provides temporal and spatial information to aid in the identification of GCN5 targets in the developing flower.

doi:10.1016/j.ydbio.2008.05.466

Program/Abstract # 486
Morphogenesis, meristems and maize: Genetic regulation of inflorescence development in plants
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Organogenesis in plants is controlled by meristems. Meristems are organized groups of cells analogous to animal "stem cells" that divide and differentiate to give rise to all of the organs of the plant. In particular, axillary or lateral meristems give rise to branches and flowers and therefore play a fundamental role in plant morphogenesis and reproduction. My lab focuses on the initiation of axillary meristems in the inflorescence (flowering branches) of the genetic model organism, maize. We have shown that the plant growth hormone, auxin, which plays a critical role in cell division, cell expansion and polar growth, is required for axillary meristem initiation during maize inflorescence development. We have identified and characterized a large class of mutants, called "*barren inflorescence*", which are defective in the initiation of axillary meristems. Cloning of these genes by our lab and others has discovered genes required for auxin biosynthesis, transport and response. Analysis of the genetic, molecular, cell biology and biochemical interactions between these genes has led to the elucidation of a genetic network regulating axillary meristem initiation in the maize inflorescence. This research was funded by NSF IOB-0416616 and USDA 2007-03036.

doi:10.1016/j.ydbio.2008.05.467

Program/Abstract # 487
Vesicular trafficking and cell expansion during maize leaf development
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Maize leaves grow in a predictable and repetitive pattern from the shoot apical meristem. Cell shapes in maize leaves directly reflect the history of division orientation relative to directional cell expansion during early development and it has been shown that the balance of division and expansion contributes to the final leaf shape. We are interested in understanding how these growth processes are regulated and have taken a forward genetics approach to identify mutants with altered cell shapes and sizes due to lesions in genes that regulate division and/or expansion. A screen identified the *Warty1* (*Wty1*) locus, which results in abnormal cell growth when it is mutated. Transposon tagging showed that this locus encodes ZmRAB2A1, a highly conserved, small GTPase. Homologous Rab2 proteins across diverse eukaryotes are known to function in vesicular trafficking within a restricted ER and Golgi cellular compartment. Using the recently released maize genome sequence, we classified 47 maize RABS into 8 distinct sub-groups. The ZmRAB2 sub-group bears high sequence similarity to HsRab2, although the maize sub-group has more members. Phenotypic characteristics of the *wty1-0* mutant, and unique aspects of grass cell expansion, suggest that ZmRAB2A1 may have acquired monocot-specific functions. This hypothesis is supported by live-cell imaging of YFP-tagged ZmRAB2A1 trafficking in multiple compartments, including the cortical cytoplasm. This novel localization suggests diversified function of ZmRAB2A1 and implicates the vesicle trafficking pathway mediated by ZmRAB2A1 in cellular signaling during leaf expansion.

doi:10.1016/j.ydbio.2008.05.468